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(FILE 'HOME' ENTERED AT 19:28:30 ON 06 DEC 2002)

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 19:28:44 ON 06 DEC 2002

SEA THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

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3 FILE AGRICOLA
1 FILE AQUASCI
23 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
14 FILE BIOTECHNO
1 FILE CABA
34 FILE CAPLUS
2 FILE CEABA-VTB
1 FILE CEN
131 FILE DGENE
22 FILE EMBASE
9 FILE ESBIOBASE
1 FILE FEDRIP
3 FILE GENBANK
1 FILE IFIPAT
5 FILE JICST-EPLUS
13 FILE LIFESCI
16 FILE MEDLINE
5 FILE PASCAL
59 FILE SCISEARCH
5 FILE TOXCENTER
227 FILE USPATFULL
1 FILE USPAT2
1 FILE WPIDS
1 FILE WPINDEX

L1 QUE THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

FILE 'USPATFULL, DGENE, SCISEARCH, CAPLUS, BIOSIS, EMBASE, MEDLINE, BIOTECHNO, LIFESCI, ESBIOBASE, BIOTECHDS, JICST-EPLUS, PASCAL, TOXCENTER, AGRICOLA, GENBANK, CEABA-VTB, AQUASCI, CABA, CEN, FEDRIP, IFIPAT, USPAT2, WPIDS' ENTERED AT 19:31:45 ON 06 DEC 2002

L2 584 S THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
L3 324 S THERMOSTAB? AND ANCEST? AND EVOLUTI?
L4 170 S L2 AND ANCEST?
L5 154 DUP REM L4 (16 DUPLICATES REMOVED)
L6 176 S L3 AND PHYLOG?
L7 157 DUP REM L6 (19 DUPLICATES REMOVED)
L8 130 S L5 AND PHYLOG?
L9 14345 S PARSIMON? AND EVOL? AND PHYLOG?
L10 3954 S L9 AND SEQUEN? AND COMPAR?
L11 792 S L10 AND ANCEST?
L12 124 S L11 AND ENZYM?
L13 62 DUP REM L12 (62 DUPLICATES REMOVED)

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 NEWS  3  Apr 09  BEILSTEIN: Reload and Implementation of a New Subject Area
 NEWS  4  Apr 09  ZDB will be removed from STN
 NEWS  5  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
 NEWS  6  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
 NEWS  7  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS  8  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS  9  Jun 03  New e-mail delivery for search results now available
 NEWS 10  Jun 10  MEDLINE Reload
 NEWS 11  Jun 10  PCTFULL has been reloaded
 NEWS 12  Jul 02  FOREGE no longer contains STANDARDS file segment
 NEWS 13  Jul 22  USAN to be reloaded July 28, 2002;
                  saved answer sets no longer valid
 NEWS 14  Jul 29  Enhanced polymer searching in REGISTRY
 NEWS 15  Jul 30  NETFIRST to be removed from STN
 NEWS 16  Aug 08  CANCERLIT reload
 NEWS 17  Aug 08  PHARMAMarketLetter(PHARMAML) - new on STN
 NEWS 18  Aug 08  NTIS has been reloaded and enhanced
 NEWS 19  Aug 19  Aquatic Toxicity Information Retrieval (AQUIRE)
                  now available on STN
 NEWS 20  Aug 19  IFIPAT, IFICDB, and IFIUDB have been reloaded
 NEWS 21  Aug 19  The MEDLINE file segment of TOXCENTER has been reloaded
 NEWS 22  Aug 26  Sequence searching in REGISTRY enhanced
 NEWS 23  Sep 03  JAPIO has been reloaded and enhanced
 NEWS 24  Sep 16  Experimental properties added to the REGISTRY file
 NEWS 25  Sep 16  Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 26  Sep 16  CA Section Thesaurus available in CAPLUS and CA
 NEWS 27  Oct 01  CASREACT Enriched with Reactions from 1907 to 1985
 NEWS 28  Oct 21  EVENTLINE has been reloaded
 NEWS 29  Oct 24  BEILSTEIN adds new search fields
 NEWS 30  Oct 24  Nutraceuticals International (NUTRACEUT) now available on STN
 NEWS 31  Oct 25  MEDLINE SDI run of October 8, 2002
 NEWS 32  Nov 18  DKILIT has been renamed APOLLIT
 NEWS 33  Nov 25  More calculated properties added to REGISTRY
 NEWS 34  Dec 02  TIBKAT will be removed from STN
 NEWS 35  Dec 04  CSA files on STN

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               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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=> index bioscience medicine
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FULL ESTIMATED COST	0.21	0.21

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67 FILES IN THE FILE LIST IN STNINDEX

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=> s thermosta? and evoluti? and dehydrogenas?

3	FILE AGRICOLA
1	FILE AQUASCI
23	FILE BIOSIS
6	FILE BIOTECHABS
6	FILE BIOTECHDS
14	FILE BIOTECHNO
1	FILE CABA
34	FILE CAPLUS
2	FILE CEABA-VTB
1	FILE CEN
131	FILE DGENE
22	FILE EMBASE
9	FILE ESBIOBASE

33 FILES SEARCHED...

1	FILE FEDRIP
3	FILE GENBANK
1	FILE IFIPAT
5	FILE JICST-EPLUS
13	FILE LIFESCI
16	FILE MEDLINE
5	FILE PASCAL
59	FILE SCISEARCH

57 FILES SEARCHED...

5	FILE TOXCENTER
227	FILE USPATFULL
1	FILE USPAT2
1	FILE WPIDS
1	FILE WPINDEX

26 FILES HAVE ONE OR MORE ANSWERS, 67 FILES SEARCHED IN STNINDEX

L1 QUE THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

=> d rank

F1	227	USPATFULL
F2	131	DGENE
F3	59	SCISEARCH

```
F4          34   CAPLUS
F5          23   BIOSIS
F6          22   EMBASE
F7          16   MEDLINE
F8          14   BIOTECHNO
F9          13   LIFESCI
F10          9   ESBIOBASE
F11          6   BIOTECHABS
F12          6   BIOTECHDS
F13          5   JICST-EPLUS
F14          5   PASCAL
F15          5   TOXCENTER
F16          3   AGRICOLA
F17          3   GENBANK
F18          2   CEABA-VTB
F19          1   AQUASCI
F20          1   CABA
F21          1   CEN
F22          1   FEDRIP
F23          1   IFIPAT
F24          1   USPAT2
F25          1   WPIDS
F26          1   WPINDEX


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=> s thermosta? and evoluti? and dehydrogenas?
  11 FILES SEARCHED...
L2   584 THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

=> s thermostab? and ancest? and evoluti?
L3   324 THERMOSTAB? AND ANCEST? AND EVOLUTI?

=> s l2 and ancest?
L4   170 L2 AND ANCEST?

=> dup rem l4
DUPLICATE IS NOT AVAILABLE IN 'DGENE, GENBANK, FEDRIP'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L4
L5   154 DUP REM L4 (16 DUPLICATES REMOVED)

=> s l3 and phylog?
L6   176 L3 AND PHYLOG?

=> dup rem l6
DUPLICATE IS NOT AVAILABLE IN 'DGENE, GENBANK, FEDRIP'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE

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PROCESSING COMPLETED FOR L6
L7          157 DUP REM L6 (19 DUPLICATES REMOVED)

=> d his

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     INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI,
     BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,
     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB,
     DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 19:28:44 ON
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               SEA THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
              ---------
                3   FILE AGRICOLA
                1   FILE AQUASCI
               23   FILE BIOSIS
                6   FILE BIOTECHABS
                6   FILE BIOTECHDS
               14   FILE BIOTECHNO
                1   FILE CABA
               34   FILE CAPLUS
                2   FILE CEABA-VTB
                1   FILE CEN
              131   FILE DGENE
               22   FILE EMBASE
                9   FILE ESBIOBASE
                1   FILE FEDRIP
                3   FILE GENBANK
                1   FILE IFIPAT
                5   FILE JICST-EPLUS
               13   FILE LIFESCI
               16   FILE MEDLINE
                5   FILE PASCAL
               59   FILE SCISEARCH
                5   FILE TOXCENTER
              227   FILE USPATFULL
                1   FILE USPAT2
                1   FILE WPIDS
                1   FILE WPINDEX
L1             QUE THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
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     FILE 'USPATFULL, DGENE, SCISEARCH, CAPLUS, BIOSIS, EMBASE, MEDLINE,
     BIOTECHNO, LIFESCI, ESBIOBASE, BIOTECHDS, JICST-EPLUS, PASCAL, TOXCENTER,
     AGRICOLA, GENBANK, CEABA-VTB, AQUASCI, CABA, CEN, FEDRIP, IFIPAT, USPAT2,
     WPIDS' ENTERED AT 19:31:45 ON 06 DEC 2002
L2          584 S THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
L3          324 S THERMOSTAB? AND ANCEST? AND EVOLUTI?
L4          170 S L2 AND ANCEST?
L5          154 DUP REM L4 (16 DUPLICATES REMOVED)
L6          176 S L3 AND PHYLOG?
L7          157 DUP REM L6 (19 DUPLICATES REMOVED)

=> s l5 and phylog?
L8         130 L5 AND PHYLOG?

=> d ti l8

L8   ANSWER 1 OF 130  USPATFULL
TI     Non-stochastic generation of genetic vaccines


=> d ti l8 1-130
```

L8 ANSWER 1 OF 130 USPATFULL
TI Non-stochastic generation of genetic vaccines

L8 ANSWER 2 OF 130 USPATFULL
TI Directed **evolution** of novel binding proteins

L8 ANSWER 3 OF 130 USPATFULL
TI Method for improving **thermostability** of proteins, proteins having **thermostability** improved by the method and nucleic acids encoding the proteins

L8 ANSWER 4 OF 130 USPATFULL
TI Biosensors, reagents and diagnostic applications of directed **evolution**

L8 ANSWER 5 OF 130 USPATFULL
TI Full-length human cDNAs encoding potentially secreted proteins

L8 ANSWER 6 OF 130 USPATFULL
TI Barley gene for Thioredoxin and NADP-thioredoxin reductase

L8 ANSWER 7 OF 130 USPATFULL
TI GENE DISCOVERY THROUGH COMPARISONS OF NETWORKS OF STRUCTURAL AND FUNCTIONAL RELATIONSHIPS AMONG KNOWN GENES AND PROTEINS

L8 ANSWER 8 OF 130 USPATFULL
TI Identification of genetic components of drug response

L8 ANSWER 9 OF 130 USPATFULL
TI Gene sequence variations with utility in determining the treatment of disease, in genes relating to drug processing

L8 ANSWER 10 OF 130 USPATFULL
TI Proteins involved in the synthesis and assembly of O-antigen in Pseudomonas aeruginosa

L8 ANSWER 11 OF 130 USPATFULL
TI Ethanol production in gram-positive microbes

L8 ANSWER 12 OF 130 USPATFULL
TI Directed **evolution** of novel binding proteins

L8 ANSWER 13 OF 130 USPATFULL
TI Directed **evolution** of novel binding proteins

L8 ANSWER 14 OF 130 USPATFULL
TI Ethanol production by recombinant hosts

L8 ANSWER 15 OF 130 USPATFULL
TI Ethanol production by recombinant hosts

L8 ANSWER 16 OF 130 USPATFULL
TI Ethanol production in Gram-positive microbes

L8 ANSWER 17 OF 130 USPATFULL
TI Ethanol production by recombinant hosts

L8 ANSWER 18 OF 130 USPATFULL
TI Directed **evolution** of novel binding proteins

L8 ANSWER 19 OF 130 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 149 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 150 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 151 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 152 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 153 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

L5 ANSWER 154 OF 154 DGENE (C) 2002 THOMSON DERWENT
TI Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -

=> d l8 3, 13, 19, 66 ibib abs

L8 ANSWER 3 OF 130 USPATFULL

ACCESSION NUMBER:	2002:251150 USPATFULL
TITLE:	Method for improving **thermostability** of proteins, proteins having **thermostability** improved by the method and nucleic acids encoding the proteins
INVENTOR(S):	Yamagishi, Akihiko, Itabashi-Ku, JAPAN
PATENT ASSIGNEE(S):	AJINOMOTO CO., INC., Chuo-Ku, JAPAN (non-U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002137094	A1	20020926	
APPLICATION INFO.:	US 2001-897107	A1	20010703	(9)

	NUMBER	DATE
PRIORITY INFORMATION:	JP 2000-201920	20000704
	JP 2001-164332	20010531

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	OBLON SPIVAK MCCLELLAND MAIER & NEUSTADT PC, FOURTH FLOOR, 1755 JEFFERSON DAVIS HIGHWAY, ARLINGTON, VA, 22202
NUMBER OF CLAIMS:	16
EXEMPLARY CLAIM:	1

NUMBER OF DRAWINGS: 13 Drawing Page(s)
LINE COUNT: 1547
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides a method for improving **thermostability** of proteins, proteins having improved **thermostability**, nucleic acids encoding the proteins and host cells producing the proteins improved in **thermostability**.

The method for improving **thermostability** of protein comprises:

(i) comparing amino acid sequences of proteins derived from two or more species which **evolutionarily** correspond to each other in a **phylogenetic** tree,

(ii) estimating an amino acid sequence of an **ancestral** protein corresponding to the amino acid sequences compared in step (i),

(iii) and comparing the amino acid residues in the amino acid sequence in one of the proteins compared in step (i) with amino acid residues at a corresponding position in the **ancestral** protein estimated in step (ii), and replacing one or more of the amino acid residues different from those of the **ancestral** protein with the same amino acid residues as those of the **ancestral** protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L8 ANSWER 13 OF 130 USPATFULL
ACCESSION NUMBER: 96:101466 USPATFULL
TITLE: Directed **evolution** of novel binding proteins
INVENTOR(S): Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Roberts, Bruce L., Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur C., Newton, MA, United States
Kent, Rachel B., Boxborough, MA, United States
PATENT ASSIGNEE(S): Protein Engineering Corporation, Cambridge, MA, United States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 5571698		19961105	
APPLICATION INFO.:	US 1993-57667		19930618	(8)

DISCLAIMER DATE: 20100629
RELATED APPLN. INFO.: Continuation of Ser. No. US 1991-664989, filed on 1 Mar 1991, now patented, Pat. No. US 5223409 which is a continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, now abandoned which is a continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, now abandoned
DOCUMENT TYPE: Utility
FILE SEGMENT: Granted
PRIMARY EXAMINER: Ulm, John
LEGAL REPRESENTATIVE: Cooper, Iver P.
NUMBER OF CLAIMS: 83
EXEMPLARY CLAIM: 1
NUMBER OF DRAWINGS: 16 Drawing Figure(s); 16 Drawing Page(s)
LINE COUNT: 15323
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses

bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L8 ANSWER 19 OF 130 DGENE (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: AAE21437 peptide DGENE
TITLE: Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -
INVENTOR: Yamagishi A
PATENT ASSIGNEE: (AJIN)AJINOMOTO CO INC.
PATENT INFO: EP 1182253 A2 20020227 73p
APPLICATION INFO: EP 2001-115642 20010703
PRIORITY INFO: JP 2000-201920 20000704
JP 2001-164332 20010531
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-294076 [34]
AN AAE21437 peptide DGENE
AB The invention relates to a method for improving **thermostability** of proteins. The method involves comparing amino acid sequences derived from two or more species which **evolutionarily** correspond to each other in **phylogenetic** tree; estimating amino acid sequence of **ancestral** protein and replacing amino acids of desired protein, which differ from those of **ancestral** protein with the same amino acids of **ancestral** protein. The method is used for improving **thermostability** of proteins preferably 3-isopropylmalate **dehydrogenase** (IPMDH) and isocitrate **dehydrogenase** (ICDH). The invention also relates to a protein having an improved **thermostability** and a nucleic acid encoding such protein. The present sequence is Sulfolobus sp. strain 7 IPMDH peptide variant. Note: The present sequence is not shown in the specification but is derived from Sulfolobus sp. strain 7 IPMDH peptide referred as SEQ ID NO: 4 (AAE21339) and shown in Fig 2 of the specification.

L8 ANSWER 66 OF 130 DGENE (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: AAE21390 peptide DGENE
TITLE: Improving protein **thermostability** of protein by estimating amino acid sequence of **ancestral** protein (AP), and replacing amino acids of desired protein, which differ from those of AP with the same amino acids of AP -
INVENTOR: Yamagishi A
PATENT ASSIGNEE: (AJIN)AJINOMOTO CO INC.
PATENT INFO: EP 1182253 A2 20020227 73p
APPLICATION INFO: EP 2001-115642 20010703
PRIORITY INFO: JP 2000-201920 20000704
JP 2001-164332 20010531
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2002-294076 [34]
AN AAE21390 peptide DGENE
AB The invention relates to a method for improving **thermostability** of proteins. The method involves comparing amino acid sequences derived from two or more species which **evolutionarily** correspond to

each other in **phylogenetic** tree; estimating amino acid sequence of **ancestral** protein and replacing amino acids of desired protein, which differ from those of **ancestral** protein with the same amino acids of **ancestral** protein. The method is used for improving **thermostability** of proteins preferably 3-isopropylmalate **dehydrogenase** (IPMDH) and isocitrate **dehydrogenase** (ICDH). The invention also relates to a protein having an improved **thermostability** and a nucleic acid encoding such protein. The present sequence is Agrobacterium tumefaciens IPMDH peptide.

=> d l5 9 42 44 45 ibib abs

L5 ANSWER 9 OF 154 USPATFULL

ACCESSION NUMBER:	2002:149300 USPATFULL
TITLE:	Enhanced protein **thermostability** and temperature resistance
INVENTOR(S):	Robb, Frank T., Silver Spring, MD, UNITED STATES Laksanalamai, Pongpan, Baltimore, MD, UNITED STATES
PATENT ASSIGNEE(S):	UNIVERSITY OF MARYLAND BIOTECHNOLOGY INSTITUTE (U.S. corporation)

	NUMBER	KIND	DATE
PATENT INFORMATION:	US 2002077459	A1	20020620
APPLICATION INFO.:	US 2001-835909	A1	20010416 (9)

	NUMBER	DATE
PRIORITY INFORMATION:	US 2000-197274P	20000414 (60)

DOCUMENT TYPE:	Utility
FILE SEGMENT:	APPLICATION
LEGAL REPRESENTATIVE:	Steven J. Hultquist, Intellectual Property/Technology Law, P.O. Box 14329, Research Triangle Park, NC, 27709
NUMBER OF CLAIMS:	30
EXEMPLARY CLAIM:	1
NUMBER OF DRAWINGS:	8 Drawing Page(s)
LINE COUNT:	829

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Small heat shock proteins, e.g., Pyrococcus fuiosus (Pfu-sHSP), confer thermotolerance on cellular cultures and on proteins in cellular extracts during prolonged incubation at elevated temperature, demonstrating the ability to protect cellular proteins and maintain cellular viability under heat stress conditions. Such heat shock proteins are effective to combat enzymatic aggregation and intracellular precipitation during heat stress, and thereby enable enhancement of the utility and stability of enzymes in various applications, e.g., Taq polymerase in PCR applications, digestive enzymes in microbial degradative applications, etc.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 42 OF 154 SCISEARCH COPYRIGHT 2002 ISI (R)

ACCESSION NUMBER:	94:62030 SCISEARCH
THE GENUINE ARTICLE:	MU988
TITLE:	CHARACTERIZATION OF AN **ANCESTRAL** TYPE OF PYRUVATE FERREDOXIN OXIDOREDUCTASE FROM THE HYPERTHERMOPHILIC BACTERIUM, THERMOTOGA-MARITIMA
AUTHOR:	BLAMEY J M; ADAMS M W W (Reprint)
CORPORATE SOURCE:	UNIV GEORGIA, DEPT BIOCHEM, ATHENS, GA, 30602 (Reprint); UNIV GEORGIA, DEPT BIOCHEM, ATHENS, GA, 30602; UNIV GEORGIA, CTR METALLOENZYME STUDIES, ATHENS, GA, 30602
COUNTRY OF AUTHOR:	USA
SOURCE:	BIOCHEMISTRY, (01 FEB 1994) Vol. 33, No. 4, pp. 1000-1007.

ISSN: 0006-2960.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 36

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The hyperthermophilic bacterium, Thermotoga maritima, is a strict anaerobe that grows up to 90-degrees-C by carbohydrate fermentation. We report here on its pyruvate ferredoxin oxidoreductase (POR), the enzyme that catalyzes the oxidation of pyruvate to acetyl-CoA, the terminal oxidation step in the conversion of glucose to acetate. T. maritima POR was purified to electrophoretic homogeneity under strictly anaerobic conditions. It has a molecular weight of 113 000 and comprises four dissimilar subunits with M(r) values of approximately 43 000, 34 000, 23 000, and 13 000. It contains thiamine pyrophosphate (TPP) and at least two ferredoxin-type [4Fe-4S] clusters per molecule, as determined by iron analysis and EPR.spectroscopy. CoASH was absolutely required for pyruvate oxidation activity, while the addition of TPP was stimulatory. The apparent K(m) values at 80-degrees-C for pyruvate, CoASH, and TPP were 14.5, 0.34, and 0.043 mM; respectively, and the corresponding apparent V(m) values ranged from 154 to 170 mumol of pyruvate oxidized/min/mg (units/mg). The apparent K(m) and V(m), values for T. maritima ferredoxin, the proposed physiological electron carrier for POR, were 26 muM and 280 units/mg, respectively. POR did not use 2-oxoglutarate, phenyl pyruvate, or indolyl pyruvate as substrates. The enzyme was extremely **thermostable**: the temperature optimum for pyruvate oxidation was above 90-degrees-C, and the time for a 50% loss of activity (t50%) at 80-degrees-C (under anaerobic conditions) was 15 h. The enzyme was also very sensitive to inactivation by oxygen, with a t50% in air at 25-degrees-C of 70 min. Sodium nitrite was a weak inhibitor of POR activity (K(i) = 54 mM), while carbon monoxide (320 muM), sodium cyanide (20 mM), sodium fluoride (5 mM), and or sodium azide (2.5 mM) had no inhibitory effect. This is the first POR to be purified from a hyperthermophilic bacterium. Interestingly, its molecular properties are more similar to those of the POR from a hyperthermophilic archaeon than to those of PORs from mesophilic bacteria. The **evolutionary** significance of this is discussed.

L5 ANSWER 44 OF 154 SCISEARCH COPYRIGHT 2002 ISI (R)DUPLICATE 5
ACCESSION NUMBER: 92:735335 SCISEARCH
THE GENUINE ARTICLE: KC936
TITLE: MALATE-**DEHYDROGENASE** (SMDH) IN AMAZON CICHLID FISHES - **EVOLUTIONARY** FEATURES
AUTHOR: FARIAS I P (Reprint); DEALMEIDAVAL V M F
CORPORATE SOURCE: FDN UNIV AMAZONAS, MINI CAMPUS ICB, ESTRADO CONTORNO S-N, BR-69000 MANAUS, AMAZONAS, BRAZIL (Reprint); INST NACL PESQUISAS, BR-69083 MANAUS, AMAZONAS, BRAZIL
COUNTRY OF AUTHOR: BRAZIL
SOURCE: COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY B-COMPARATIVE BIOCHEMISTRY, (DEC 1992) Vol. 103, No. 4, pp. 939-943. ISSN: 0305-0491.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 40

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB 1. The sMDH isozyme system was studied in five species of cichlid fishes found in the Amazon hydrographic basin (Astronotus ocellatus, Cichla monoculus, Geophagus cff harreri, Cichlassoma severum and Mesonauta insignis). All studied specimens presented a six-banded electrophoretic pattern, suggesting the existence of three gene loci (sMDH-A*, sMDH-B1* and sMDH-B2*).

2. Klebe's serial dilutions, **thermostability** tests and tissue specificity performed on the sMDH of studied species indicated no divergence between B1* and B2* loci products, suggesting that these genes

probably undergo the same regulatory gene action and that the duplication event occurred recently, after A* and B* divergence.

3. The appearance of the same characteristics in all specimens, and the chromosomic picture of the family, suggest the occurrence of an event of duplication "in tandem" in the **ancestors** of Amazon cichlids.

L5 ANSWER 45 OF 154 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 6
ACCESSION NUMBER: 1989:52141 CAPLUS
DOCUMENT NUMBER: 110:52141
TITLE: Duck lens .epsilon.-crystallin and lactate **dehydrogenase** B4 are identical: a single-copy gene product with two distinct functions
AUTHOR(S): Hendriks, Wiljan; Mulders, John W. M.; Bibby, Michael A.; Slingsby, Christine; Bloemendal, Hans; De Jong, Wilfried W.
CORPORATE SOURCE: Dep. Biochem., Univ. Nijmegen, Nijmegen, 6500 HB, Neth.
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1988), 85(19), 7114-18
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To investigate whether duck lens .epsilon.-crystallin and duck heart lactate **dehydrogenase** (LDH) B4 are the product of the same gene, the cDNA clones of duck .epsilon.-crystallin were isolated and sequenced. These clones demonstrate that there is a single-copy Ldh-B gene in duck and in chicken. In the duck lens, this gene is overexpressed, and its product is subject to posttranslational modification. Reconstruction of the **evolutionary** history of the LDH protein family reveals that the mammalian Ldh-C gene most probably originated from an **ancestral** Ldh-A gene and that the amino acid replacement rate in LDH-C is .apprx.4-fold the rate in LDH-A. Mol. modeling of LDH-B sequences shows that the increased **thermostability** of the avian tetramer might be explained by mutations that increase the no. of ion pairs. Furthermore, the replacement of bulky side chains by glycines on the corners of the duck protein suggests an adaptation to facilitate close packing in the lens.

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(FILE 'HOME' ENTERED AT 19:28:30 ON 06 DEC 2002)

INDEX 'ADISALERTS, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 19:28:44 ON 06 DEC 2002

SEA THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

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3 FILE AGRICOLA
1 FILE AQUASCI
23 FILE BIOSIS
6 FILE BIOTECHABS
6 FILE BIOTECHDS
14 FILE BIOTECHNO
1 FILE CABA
34 FILE CAPLUS
2 FILE CEABA-VTB
1 FILE CEN
131 FILE DGENE
22 FILE EMBASE
9 FILE ESBIOBASE
1 FILE FEDRIP
3 FILE GENBANK

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                1   FILE IFIPAT
                5   FILE JICST-EPLUS
               13   FILE LIFESCI
               16   FILE MEDLINE
                5   FILE PASCAL
               59   FILE SCISEARCH
                5   FILE TOXCENTER
              227   FILE USPATFULL
                1   FILE USPAT2
                1   FILE WPIDS
                1   FILE WPINDEX
L1               QUE THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
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     FILE 'USPATFULL, DGENE, SCISEARCH, CAPLUS, BIOSIS, EMBASE, MEDLINE,
     BIOTECHNO, LIFESCI, ESBIOBASE, BIOTECHDS, JICST-EPLUS, PASCAL, TOXCENTER,
     AGRICOLA, GENBANK, CEABA-VTB, AQUASCI, CABA, CEN, FEDRIP, IFIPAT, USPAT2,
     WPIDS' ENTERED AT 19:31:45 ON 06 DEC 2002
L2            584 S THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?
L3            324 S THERMOSTAB? AND ANCEST? AND EVOLUTI?
L4            170 S L2 AND ANCEST?
L5            154 DUP REM L4 (16 DUPLICATES REMOVED)
L6            176 S L3 AND PHYLOG?
L7            157 DUP REM L6 (19 DUPLICATES REMOVED)
L8            130 S L5 AND PHYLOG?

=> s parsimon? and evol? and phylog?
L9         14345 PARSIMON? AND EVOL? AND PHYLOG?

=> s l9 and sequen? and compar?
   2 FILES SEARCHED...
   9 FILES SEARCHED...
  14 FILES SEARCHED...
  16 FILES SEARCHED...
L10         3954 L9 AND SEQUEN? AND COMPAR?

=> s l10 and ancest?
L11          792 L10 AND ANCEST?

=> s l11 and enzym?
  14 FILES SEARCHED...
L12          124 L11 AND ENZYM?

=> dup rem l12
DUPLICATE IS NOT AVAILABLE IN 'DGENE, GENBANK, FEDRIP'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L12
L13            62 DUP REM L12 (62 DUPLICATES REMOVED)

=> d ti l13 1-62

L13  ANSWER 1 OF 62  USPATFULL                              DUPLICATE 1
TI     Method for improving thermostability of proteins, proteins having
       thermostability improved by the method and nucleic acids encoding the
       proteins

L13  ANSWER 2 OF 62  USPATFULL                              DUPLICATE 2
TI     DNA-BASED TRANSPOSON SYSTEM FOR THE INTRODUCTION OF NUCLEIC ACID INTO
       DNA OF A CELL

L13  ANSWER 3 OF 62  CAPLUS  COPYRIGHT 2002 ACS            DUPLICATE 3
TI   Improving thermostability of 3-isopropylmalate dehydrogenase and
     isocitrate dehydrogenase by replacement with amino acid residues of
     ancestral enzymes of thermophilic species
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L13 ANSWER 4 OF 62 USPATFULL
TI Method of modifying the content of cottonseed oil

L13 ANSWER 5 OF 62 USPATFULL
TI Ehrlichia chaffeensis 28 kDa outer membrane protein multigene family

L13 ANSWER 6 OF 62 USPATFULL
TI Gene **sequence** variances in genes related to folate metabolism having utility in determining the treatment of disease

L13 ANSWER 7 OF 62 USPATFULL
TI Identification of genetic components of drug response

L13 ANSWER 8 OF 62 USPATFULL
TI Polypeptides associated with alterations in bone density

L13 ANSWER 9 OF 62 USPATFULL
TI Pharmacological targeting of mRNA cap formation for treatment of parasitic infections

L13 ANSWER 10 OF 62 USPATFULL
TI Stable envelope proteins for retroviral, viral and liposome vectors and use in gene drug therapy

L13 ANSWER 11 OF 62 USPATFULL
TI Swine hepatitis E virus and uses thereof

L13 ANSWER 12 OF 62 USPATFULL
TI Nucleotide **sequences** of HIV-1 type (or subtype) O retrovirus antigens

L13 ANSWER 13 OF 62 USPATFULL
TI Nucleic acids encoding a novel family of TGF-.beta. binding proteins from humans

L13 ANSWER 14 OF 62 USPATFULL
TI Application of protein structure predictions

L13 ANSWER 15 OF 62 USPATFULL
TI Methods of surveying for CC (Beta) chemokine receptor variants and their association with HIV-1 transmission and/or disease progression

L13 ANSWER 16 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI alpha-Proteobacterial relationship of apicomplexan lactate and malate dehydrogenases.

L13 ANSWER 17 OF 62 MEDLINE
TI **Phylogenetic** relationships between the six superoxide dismutase proteins (FeSOD) of Trichomonas vaginalis and FeSOD6 genetic diversity.

L13 ANSWER 18 OF 62 USPATFULL
TI Gene **sequence** variations with utility in determining the treatment of disease, in genes relating to drug processing

L13 ANSWER 19 OF 62 USPATFULL
TI Method of detecting genetic polymorphisms using over represented **sequences**

L13 ANSWER 20 OF 62 USPATFULL
TI ABO histo-blood group O alleles of the baboon

L13 ANSWER 21 OF 62 USPATFULL
TI Diagnostic methods for Cyclospora

L13 ANSWER 22 OF 62 USPATFULL

TI Insertion **sequence** from a virulent isolate of Burkholderia cepacia, and diagnostic and identification procedures based thereon

L13 ANSWER 23 OF 62 PASCAL COPYRIGHT 2002 INIST-CNRS. ALL RIGHTS RESERVED.
TIEN Molecular **evolution** of the Chlamydiaceae

L13 ANSWER 24 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 4
TI **Comparative** genomics and bioenergetics

L13 ANSWER 25 OF 62 USPATFULL
TI Method to determine predisposition to hypertension

L13 ANSWER 26 OF 62 USPATFULL
TI Unique associated Kaposi's sarcoma virus **sequences** and uses thereof

L13 ANSWER 27 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 5
TI Implications of chloroplast DNA restriction site variation for systematics of Acacia (Fabaceae : Mimosoideae)

L13 ANSWER 28 OF 62 USPATFULL
TI Predicting folded structures of proteins

L13 ANSWER 29 OF 62 USPATFULL
TI Kaposi's sarcoma-associated herpesvirus (KSHV) glycoprotein B (GB) and uses thereof

L13 ANSWER 30 OF 62 USPATFULL
TI Kaposi's sarcoma-associated herpesvirus (KSHV) interleukin 6 (IL-6) and uses thereof

L13 ANSWER 31 OF 62 CABA COPYRIGHT 2002 CABI
TI Mitochondrial DNA **phylogeny** and the **evolution** of host-plant use in Palearctic Chrysolina (Coleoptera, Chrysomelidae) leaf beetles.

L13 ANSWER 32 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 6
TI Molecular systematics of cytochrome oxidase I and 16S from Neochlamisus leaf beetles and the importance of sampling.

L13 ANSWER 33 OF 62 USPATFULL
TI Kaposi's sarcoma-associated herpesvirus (KSHV) viral macrophage inflammatory protein-1.alpha. II (vMIP-1.alpha. II) and uses thereof

L13 ANSWER 34 OF 62 USPATFULL
TI Kaposi's sarcoma-associated herpesvirus (KSHV) interleukin 6 (IL-6) and uses thereof

L13 ANSWER 35 OF 62 USPATFULL
TI Simplified hybrid seed production by latent diploid parthenogenesis and parthenote cleavage

L13 ANSWER 36 OF 62 USPATFULL
TI Kaposi's sarcoma-associated herpes virus (KSHV) interferon consensus **sequence** binding protein (ICSBP) and uses thereof

L13 ANSWER 37 OF 62 USPATFULL
TI Hepatitis-C virus testing

L13 ANSWER 38 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 7
TI Chloroplast DNA restriction site variation and **phylogeny** of the Berberidaceae

L13 ANSWER 39 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 8

TI Parallel **evolution** of glucosinolate biosynthesis inferred from congruent nuclear and plastid gene **phylogenies**

L13 ANSWER 40 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 9
TI A unique fungal lysine biosynthesis **enzyme** shares a common **ancestor** with tricarboxylic acid cycle and leucine biosynthetic **enzymes** found in diverse organisms

L13 ANSWER 41 OF 62 MEDLINE
TI **Phylogenetic** relationships of the glycolytic **enzyme**, glyceraldehyde-3-phosphate dehydrogenase, from parabasalid flagellates.

L13 ANSWER 42 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Intraspecific **phylogeography** of the Cape galaxias form South Africa: Evidence from mitochondrial DNA **sequences**.

L13 ANSWER 43 OF 62 MEDLINE
TI **Phylogenetic** analyses of the rbcL **sequences** from haptophytes and heterokont algae suggest their chloroplasts are unrelated.

L13 ANSWER 44 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 10
TI Detection of convergent and parallel **evolution** at the amino acid **sequence** level.

L13 ANSWER 45 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI A **phylogenetic** analysis of body size **evolution** and biogeography in chuckwallas (Sauromalus) and other iguanines.

L13 ANSWER 46 OF 62 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI **Phylogenetic** reconstruction of the Felidae using 16S rRNA and NADH-5 mitochondrial genes.

L13 ANSWER 47 OF 62 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.
TI **Phylogenetic** reconstruction of the Felidae using 16S rRNA and NADH-5 mitochondrial genes

L13 ANSWER 48 OF 62 USPATFULL
TI DNA encoding glutamate gated chloride channels

L13 ANSWER 49 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 11
TI Molecular **evolution** of maize catalases and their relationship to other eukaryotic and prokaryotic catalases.

L13 ANSWER 50 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 12
TI PRIMARY STRUCTURE AND **PHYLOGENETIC**-RELATIONSHIPS OF GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE GENES OF FREE-LIVING AND PARASITIC DIPLOMONAD FLAGELLATES

L13 ANSWER 51 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R)
TI DIRECT EVIDENCE FOR SECONDARY LOSS OF MITOCHONDRIA IN ENTAMOEBA-HISTOLYTICA

L13 ANSWER 52 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 13
TI GENETIC-EVIDENCE FOR A HANTAVIRUS ENZOOTIC IN DEER MICE (PEROMYSCUS-MANICULATUS) CAPTURED A DECADE BEFORE THE RECOGNITION OF HANTAVIRUS PULMONARY SYNDROME

L13 ANSWER 53 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R)
TI TRACING PATERNAL **ANCESTRY** IN MICE, USING THE Y-LINKED, SEX-DETERMINING LOCUS, SRY

L13 ANSWER 54 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Reconstruction of **ancestral sequences** by the

inferential method, a tool for protein engineering studies.

L13 ANSWER 55 OF 62 USPATFULL
TI Genetic test for hereditary neuromuscular disease

L13 ANSWER 56 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI **Phylogenetic** Relationships in the honeybee (Genus Apis) as determined by the **sequence** of the cytochrome oxidase II region of mitochondrial DNA.

L13 ANSWER 57 OF 62 MEDLINE DUPLICATE 14
TI **Evolution** of RNA polymerases and branching patterns of the three major groups of Archaebacteria.

L13 ANSWER 58 OF 62 MEDLINE DUPLICATE 15
TI **Phylogenetic** analysis of the RNA polymerases of Trypanosoma brucei, with special reference to class-specific transcription.

L13 ANSWER 59 OF 62 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 16
TI Structural and **evolutionary comparisons** of four alleles of the mouse Igk-J locus which encodes immunoglobulin kappa light chain joining (J.kappa.) segments

L13 ANSWER 60 OF 62 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 17
TI **Phylogenetic** implications of chloroplast DNA restriction site variation in the Mutisieae (Asteraceae)

L13 ANSWER 61 OF 62 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 18
TI Mitochondrial DNA **evolution** in the genus Equus

L13 ANSWER 62 OF 62 FEDRIP COPYRIGHT 2002 NTIS
TI **EVOLUTIONARY** RELATIONSHIPS AND GENETIC CHARACTERIZATION OF PSYLLID ENDOSYMBIONTS

=> d ti l13 17 23 31 39 40 41 44 49 50 54 56 57 62 ibib abs

L13 ANSWER 17 OF 62 MEDLINE
TI **Phylogenetic** relationships between the six superoxide dismutase proteins (FeSOD) of Trichomonas vaginalis and FeSOD6 genetic diversity.
ACCESSION NUMBER: 2002205849 MEDLINE
DOCUMENT NUMBER: 21936988 PubMed ID: 11938694
TITLE: **Phylogenetic** relationships between the six superoxide dismutase proteins (FeSOD) of Trichomonas vaginalis and FeSOD6 genetic diversity.
AUTHOR: Hwang U W; Shin K S; Ryu J S; Min D Y; Ahn M H
CORPORATE SOURCE: Department of Biology, Teachers College, Kyungpook National University, Taegu 702-701, Korea & Department of Parasitology, Yonsei University College of Medicine, Seoul 120-752, Korea.
SOURCE: PARASITE, (2002 Mar) 9 (1) 37-42.
Journal code: 9437094. ISSN: 1252-607X.
PUB. COUNTRY: France
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020410
Last Updated on STN: 20020528
Entered Medline: 20020522
AB The parasitic protozoan Trichomonas vaginalis is known to contain several types of Fe-containing superoxide dismutase proteins (FeSOD). Using three different methods of **phylogenetic** analysis, maximum **parsimony** (MP), neighbor joining (NJ), and maximum likelihood (ML) methods, we examined the **phylogenetic** relationships among the

six FeSOD (FeSOD1-FeSOD6) based on their amino acid **sequences**. All the analyses consistently suggested that the six proteins formed a monophyletic group implying that they probably be originated from an **ancestral** protein form through repeated duplication events. Although MP tree was totally unresolved, the NJ and ML trees revealed that FeSOD6 placed the most basal position and thus emerged earlier than the other five gene types during the **evolution** of T. vaginalis. **Phylogenetic** relationships among the five remaining proteins were (FeSOD2, FeSOD3), (FeSOD4, (FeSOD1, FeSOD5)) although weakly supported in terms of bootstrapping values. In addition to this, we newly designed two PCR primer specifically amplifying full-length FeSOD6 gene and examined its genetic diversity among 12 T. vaginalis isolates from five countries and three continents. They had the same nucleotide **sequences** except those of three Korean isolates which showed one to three different nucleotides.

L13 ANSWER 23 OF 62 PASCAL COPYRIGHT 2002 INIST-CNRS. ALL RIGHTS RESERVED.
TIEN Molecular **evolution** of the Chlamydiaceae
ACCESSION NUMBER: 2002-0324220 PASCAL
COPYRIGHT NOTICE: Copyright .COPYRGT. 2002 INIST-CNRS. All rights reserved.
TITLE (IN ENGLISH): Molecular **evolution** of the Chlamydiaceae
AUTHOR: BUSH Robin M.; EVERETT Karin D. E.
CORPORATE SOURCE: Department of Ecology and Evolutionary Biology, University of California, Irvine, CA 92697, United States; Department of Medical Microbiology and Parasitology, College of Veterinary Medicine, University of Georgia, Athens, GA 30602, United States
SOURCE: International journal of systematic and evolutionary microbiology : (Print), (2001), 51(1), 203-220, refs. 4 p.
ISSN: 1466-5026
DOCUMENT TYPE: Journal
BIBLIOGRAPHIC LEVEL: Analytic
COUNTRY: United Kingdom
LANGUAGE: English
AVAILABILITY: INIST-9775, 354000098732670290
AN 2002-0324220 PASCAL
CP Copyright .COPYRGT. 2002 INIST-CNRS. All rights reserved.
AB **Phylogenetic** analyses of surface antigens and other chlamydial proteins were used to reconstruct the **evolution** of the Chlamydiaceae. Trees for all five coding genes [the major outer-membrane protein (MOMP), GroEL chaperonin, KDO-transferase, small cysteine-rich lipoprotein and 60 kDa cysteine-rich protein] supported the current organization of the family Chlamydiaceae, which is based on ribosomal, biochemical, serological, ecological and DNA-DNA hybridization data. Genetic distances between some species were quite large, so **phylogenies** were evaluated for robustness by **comparing** analyses of both nucleotide and protein **sequences** using a variety of algorithms (neighbour-joining, maximum-likelihood, maximum-**parsimony** with bootstrapping, and quartet puzzling). Saturation plots identified areas of the trees in which factors other than relatedness may have determined branch attachments. All nine species were clearly differentiated by distinctness ratios calculated for each gene. The distribution of virulence traits such as host and tissue tropism were mapped onto the consensus **phylogeny**. Closely related species were no more likely to share virulence characters than were more distantly related species. This **phylogenetically** disjunct distribution of virulence traits could not be explained by lateral transfer of the genes we studied, since we found no evidence for lateral gene transfer above the species level. One interpretation of this observation is that when chlamydiae gain access to a new niche, such as a new host or tissue, significant adaptation ensues and the virulence phenotype of the new species reflects adaptation to its environment more strongly than it reflects its **ancestry**.

L13 ANSWER 31 OF 62 CABA COPYRIGHT 2002 CABI
TI Mitochondrial DNA **phylogeny** and the **evolution** of host-plant use in Palearctic Chrysolina (Coleoptera, Chrysomelidae) leaf beetles.

ACCESSION NUMBER: 2002:159177 CABA
DOCUMENT NUMBER: 20023061561
TITLE: Mitochondrial DNA **phylogeny** and the **evolution** of host-plant use in Palearctic Chrysolina (Coleoptera, Chrysomelidae) leaf beetles
AUTHOR: Garin, C. F.; Juan, C.; Petitpierre, E.
CORPORATE SOURCE: Departament de Biologia, Universitat de les Illes Balears, Palma de Mallorca 07071, Spain.
SOURCE: Journal of Molecular Evolution, (1999) Vol. 48, No. 4, pp. 435-444. 46 ref.
ISSN: 0022-2844
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The genus Chrysolina consists of specialized phytophagous leaf-beetles (Coleoptera, Chrysomelidae) which feed on several plant families. There is no explicit **phylogenetic** hypothesis available for this genus, which includes 65 subgenera and more than 400 species with a wide distribution. We obtained 839-bp **sequence** data from the 16S rDNA and cytochrome oxidase subunit I (COI) mitochondrial genes. Thirty Chrysolina taxa representing eight host-plant affiliations, two species of the closely related genus Oreina, and two outgroups were sampled. These data sets were used separately and combined to obtain the mitochondrial cladogram of the group using maximum-**parsimony** and maximum-likelihood criteria. The results were **compared** to current proposals for Chrysolina systematics that are based on morphological, ecological, and karyological data. The trees obtained were in the most part congruent with the proposed **ancestral** association of Chrysolina to Lamiaceae based on chromosome number in several lineages. A minimum of five host-plant switches from the **ancestral** state inferred at the family level and two at the subclass level suggests the absence of parallel **evolution** of beetles and their host plants. Another switch leading to oligophagy at the family level was deduced to have occurred in the lineage of the subgenus Chrysolina s.str.

L13 ANSWER 39 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 8
TI Parallel **evolution** of glucosinolate biosynthesis inferred from congruent nuclear and plastid gene **phylogenies**

ACCESSION NUMBER: 1998:586918 SCISEARCH
THE GENUINE ARTICLE: 104DQ
TITLE: Parallel **evolution** of glucosinolate biosynthesis inferred from congruent nuclear and plastid gene **phylogenies**
AUTHOR: Rodman J E (Reprint); Soltis P S; Soltis D E; Sytsma K J; Karol K G
CORPORATE SOURCE: NATL SCI FDN, DIV ENVIRONM BIOL, ARLINGTON, VA 22230 (Reprint); WASHINGTON STATE UNIV, DEPT BOT, PULLMAN, WA 99164; UNIV WISCONSIN, DEPT BOT, MADISON, WI 53706; SMITHSONIAN INST, LAB MOL SYSTEMAT, WASHINGTON, DC 20560
COUNTRY OF AUTHOR: USA
SOURCE: AMERICAN JOURNAL OF BOTANY, (JUL 1998) Vol. 85, No. 7, pp. 997-1006.
Publisher: BOTANICAL SOC AMER INC, OHIO STATE UNIV-DEPT BOTANY 1735 NEIL AVE, COLUMBUS, OH 43210.
ISSN: 0002-9122.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: AGRI
LANGUAGE: English
REFERENCE COUNT: 68

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB zThe phytochemical system of mustard-oil glucosides (glucosinolates) accompanied by the hydrolytic **enzyme** myrosinase (beta-thioglucosidase), the latter usually **compartmented** in special myrosin cells, characterizes plants in 16 families of angiosperms. Traditional classifications place these taxa in many separate orders and thus imply multiple convergences in the origin of this chemical defense system. DNA **sequencing** of the chloroplast rbcL gene for representatives of all 16 families and several putative relatives, with **phylogenetic** analyses by **parsimony** and maximum likelihood methods, demonstrated instead a single major clade of mustard-oil plants and one **phylogenetic** outlier. In a further independent test, DNA **sequencing** of the nuclear 18S ribosomal RNA gene for all these exemplars has yielded the same result, a major mustard-oil clade of 15 families (Akaniaceae, Bataceae, Brassicaceae, Bretschneideraceae, Capparaceae, Caricaceae, Gyrostemonaceae, Koeberliniaceae, Limnanthaceae, Moringaceae, Pentadiplandraceae, Resedaceae, Salvadoraceae, Tovariaceae, and Tropaeolaceae) and one outlier, the genus Drypetes, traditionally placed in Euphorbiaceae. Concatenating the two gene **sequences** (for a total of 3254 nucleotides) in a data set for 33 taxa, we obtain robust support for this finding of parallel origins of glucosinolate biosynthesis. From likely cyanogenic **ancestors**, the ''mustard oil bomb'' was invented twice.

L13 ANSWER 40 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 9
TI A unique fungal lysine biosynthesis **enzyme** shares a common **ancestor** with tricarboxylic acid cycle and leucine biosynthetic **enzymes** found in diverse organisms

ACCESSION NUMBER: 1998:255672 SCISEARCH
THE GENUINE ARTICLE: ZD540
TITLE: A unique fungal lysine biosynthesis **enzyme** shares a common **ancestor** with tricarboxylic acid cycle and leucine biosynthetic **enzymes** found in diverse organisms
AUTHOR: Irvin S D (Reprint); Bhattacharjee J K
CORPORATE SOURCE: CORNELL UNIV, GENET & DEV SECT, 403 BIOTECHNOL BLDG, ITHACA, NY 14853 (Reprint); MIAMI UNIV, DEPT MICROBIOL, OXFORD, OH 45056
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF MOLECULAR EVOLUTION, (APR 1998) Vol. 46, No. 4, pp. 401-408.
Publisher: SPRINGER VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010.
ISSN: 0022-2844.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: English
REFERENCE COUNT: 30

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Fungi have **evolved** a unique alpha-aminoadipate pathway for lysine biosynthesis. The fungal-specific **enzyme** homoaconitate hydratase from this pathway is moderately similar to the aconitase-family proteins from a diverse array of taxonomic groups, which have varying modes of obtaining lysine. We have used the similarity of homoaconitate hydratase to isopropylmalate isomerase (serving in leucine biosynthesis), aconitase (from the tricarboxylic acid cycle), and iron-responsive element binding proteins (cytosolic aconitase) from fungi and other eukaryotes, eubacteria, and archaea to evaluate possible **evolutionary** scenarios for the origin of this pathway. Refined **sequence** alignments show that aconitase active site residues are highly conserved in each of the **enzymes**, and intervening **sequence** sites are quite dissimilar. This pattern suggests strong purifying selection has acted to preserve the aconitase active site residues for a common catalytic mechanism; numerous other substitutions occur due to adaptive **evolution** or simply lack of functional constraint. We hypothesize

that the similarities are the remnants of an **ancestral** gene duplication, which may not have occurred within the fungal lineage, Maximum likelihood, neighbor joining, and maximum **parsimony** **phylogenetic comparisons** show that the alpha-aminoadipate pathway **enzyme** is an outgroup to all aconitase family proteins for which **sequence** is currently available.

L13 ANSWER 41 OF 62 MEDLINE
TI **Phylogenetic** relationships of the glycolytic **enzyme**, glyceraldehyde-3-phosphate dehydrogenase, from parabasalid flagellates.
ACCESSION NUMBER: 1998360012 MEDLINE
DOCUMENT NUMBER: 98360012 PubMed ID: 9694668
TITLE: **Phylogenetic** relationships of the glycolytic **enzyme**, glyceraldehyde-3-phosphate dehydrogenase, from parabasalid flagellates.
AUTHOR: Viscogliosi E; Muller M
CORPORATE SOURCE: The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA.
CONTRACT NUMBER: AI 11942 (NIAID)
SOURCE: JOURNAL OF MOLECULAR EVOLUTION, (1998 Aug) 47 (2) 190-9. Journal code: 0360051. ISSN: 0022-2844.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF022414; GENBANK-AF022415; GENBANK-AF022416; GENBANK-AF022417; GENBANK-AF022418; GENBANK-AF022419; GENBANK-AF022420
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 20000303
Entered Medline: 19980909

AB Over 90% of the open reading frame of gap genes for glycolytic glyceraldehyde-3-phosphate dehydrogenase (GAPDH; EC 1.2.1.12) was obtained with PCR from five species of Parabasala. With gap1 from Trichomonas vaginalis obtained earlier, the data include two **sequences** each for three species. All **sequences** were colinear with T. vaginalis gap1 and shared with it as a synapomorphy a 10- to 11-residue insertion not found in any other gap and an S-loop with characteristic features of eubacterial GAPDH. All residues known to be highly conserved in this **enzyme** were present. The parabasalid **sequences** formed a robust monophyletic group in **phylogenetic** reconstructions with distance-based, maximum-**parsimony**, and maximum-likelihood methods. The two genes of the amphibian commensal, Trichomitus batrachorum, shared a common **ancestor** with the rest, which separate into two well-supported lineages. T. vaginalis and Tetratrichomonas gallinarum (both representatives of Trichomonadinae) formed one, while Monocercomonas sp. and Tritrichomonas foetus formed the other. These data agreed with and/or were close to published reconstructions based on other macromolecules. They did not support the **ancestral** position of Monocercomonas sp. proposed on the basis of morphological characteristics but confirmed an early emergence of Trichomitus batrachorum. The **sequence** pairs obtained from three species indicated either gene duplications subsequent to the divergence of the corresponding lineages or a strong gene conversion later in these lineages. The parabasalid clade was a robust part of the eubacterial radiation of GAPDH and showed no relationships to the clade that contained all other eukaryotic gap genes. The data clearly reveal that the members of this lineage use in their glycolytic pathway a GAPDH species with properties and an **evolutionary** history that are unique among all eukaryotes studied so far.

L13 ANSWER 44 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 10

TI Detection of convergent and parallel **evolution** at the amino acid **sequence** level.
ACCESSION NUMBER: 1997:268607 BIOSIS
DOCUMENT NUMBER: PREV199799560325
TITLE: Detection of convergent and parallel **evolution** at the amino acid **sequence** level.
AUTHOR(S): Zhang, Jianzhi (1); Kumar, Sudhir
CORPORATE SOURCE: (1) Inst. Molecular Evolutionary Genetics, Pennsylvania State Univ., 322 Mueller Lab., University Park, PA 16802 USA
SOURCE: Molecular Biology and Evolution, (1997) Vol. 14, No. 5, pp. 527-536.
ISSN: 0737-4038.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Adaptive **evolution** at the molecular level can be studied by detecting convergent and parallel **evolution** at the amino acid **sequence** level. For a set of homologous protein **sequences**, the **ancestral** amino acids at all interior nodes of the **phylogenetic** tree of the proteins can be statistically inferred. The amino acid sites that have experienced convergent or parallel changes on independent **evolutionary** lineages can then be identified by **comparing** the amino acids at the beginning and end of each lineage. At present, the efficiency of the methods of **ancestral sequence** inference in identifying convergent and parallel changes is unknown. More seriously, when we identify convergent or parallel changes, it is unclear whether these changes are attributable to random chance. For these reasons, claims of convergent and parallel **evolution** at the amino acid **sequence** level have been disputed. We have conducted computer simulations to assess the efficiencies of the **parsimony** and Bayesian methods of **ancestral sequence** inference in identifying convergent and parallel-change sites. Our results showed that the Bayesian method performs better than the **parsimony** method in identifying parallel changes, and both methods are inefficient in identifying convergent changes. However, the Bayesian method is recommended for estimating the number of convergent-change sites because it gives a conservative estimate. We have developed statistical tests for examining whether the observed numbers of convergent and parallel changes are due to random chance. As an example, we reanalyzed the stomach lysozyme **sequences** of foregut fermenters and found that parallel **evolution** is statistically significant, whereas convergent **evolution** is not well supported.

L13 ANSWER 49 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 11
TI Molecular **evolution** of maize catalases and their relationship to other eukaryotic and prokaryotic catalases.
ACCESSION NUMBER: 1996:365113 BIOSIS
DOCUMENT NUMBER: PREV199699087469
TITLE: Molecular **evolution** of maize catalases and their relationship to other eukaryotic and prokaryotic catalases.
AUTHOR(S): Guan, Lingqiang; Scandalios, John G. (1)
CORPORATE SOURCE: (1) Dep. Genet., Box 7164, North Carolina State University, Raleigh, NC 27695-7614 USA
SOURCE: Journal of Molecular Evolution, (1996) Vol. 42, No. 5, pp. 570-579.
ISSN: 0022-2844.
DOCUMENT TYPE: Article
LANGUAGE: English
AB We have **compared** the nucleotide and protein **sequences** of the three maize catalase genes with other plant catalases to reconstruct the **evolutionary** relationship among these catalases. These **sequences** were also **compared** with other eukaryotic and prokaryotic catalases. **Phylogenies** based on

distances and **parsimony** analysis show that all plant catalases derive from a common **ancestral** catalase gene and can be divided into three distinct groups. The first, and major, group includes maize Cat1, barley Cat1, rice CatB, and most of the dicot catalases. The second group is an apparent dicot-specific catalase group encompassing the tobacco Cat2 and tomato Cat. The third is a monocot-specific catalase class including the maize Cat3, barley Cat2, and rice CatA. The maize Cat2 gene is loosely related to the first group. The distinctive features of monocot-specific catalases are their extreme high codon bias at the third position and low degree of **sequence** similarity to other plant catalases. Similarities in the intron positions for several plant catalase genes support the conclusion of derivation from a common **ancestral** gene. The similar intron position between bean catalases and human catalase implies that the animal and plant catalases might have derived from a common progenitor gene **sequence**.

L13 ANSWER 50 OF 62 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 12
TI PRIMARY STRUCTURE AND **PHYLOGENETIC**-RELATIONSHIPS OF GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE GENES OF FREE-LIVING AND PARASITIC DIPLOMONAD FLAGELLATES

ACCESSION NUMBER: 96:584048 SCISEARCH
THE GENUINE ARTICLE: VA333
TITLE: PRIMARY STRUCTURE AND **PHYLOGENETIC**-RELATIONSHIPS OF GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE GENES OF FREE-LIVING AND PARASITIC DIPLOMONAD FLAGELLATES
AUTHOR: ROZARIO C; MORIN L; ROGER A J; SMITH M W; MULLER M (Reprint)
CORPORATE SOURCE: ROCKEFELLER UNIV, 1230 YORK AVE, NEW YORK, NY, 10021 (Reprint); ROCKEFELLER UNIV, NEW YORK, NY, 10021; UNIV PARIS 11, BIOL CELLULAIRE LAB, F-91405 ORSAY, FRANCE; DALHOUSIE UNIV, DEPT BIOCHEM, HALIFAX, NS B3H 4H7, CANADA; SALK INST BIOL STUDIES, MOL GENET LAB, SAN DIEGO, CA, 92138
COUNTRY OF AUTHOR: USA; FRANCE; CANADA
SOURCE: JOURNAL OF EUKARYOTIC MICROBIOLOGY, (JUL/AUG 1996) Vol. 43, No. 4, pp. 330-340.
ISSN: 1066-5234.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; AGRI
LANGUAGE: ENGLISH
REFERENCE COUNT: 73

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Complete nucleotide **sequences** have been established for two genes (gap1 and gap2) coding for glyceraldehyde-3-phosphate dehydrogenase (GAPDH, EC 1.2.1.12)homologs in the diplomonad Giardia lamblia. In addition, almost complete **sequences** of the GAPDH open reading frames were obtained from PCR products for two free-living diplomonad species, Trepomonas agilis and Hexamita inflata, and a parasite of Atlantic salmon, an as yet unnamed species with morphological affinities to Spironucleus. Giardia lamblia gap1 and the genes from the three other diplomonad species show high similarity to each other and to other glycolytic GAPDH genes. All amino-acyl residues known to be highly conserved in this **enzyme** are also conserved in these **sequences**. Giardia lamblia gap2 gene is more divergent and its putative translation reveals the presence of a cysteine and serine-rich insertion resembling a metal binding finger. This motif has not yet been noted in other GAPDH molecules. All **sequences** contain an S-loop signature with characteristics close to those of eukaryotes. In **phylogenetic** reconstructions based on the derived amino acid **sequences** with neighbor-joining, **parsimony** and maximum-likelihood methods the four typical GAPDH **sequences** of diplomonads cluster into a single clade. Within this clade, G. lamblia gap1 shares a common **ancestor** with the rest of the genes. The latter are more closely related to each other, indicating an early separation of the lineage leading to the genus Giardia from the lineage

encompassing the morphologically less differentiated genera, Trepomonas, Hexamita and that of the unnamed species. This result is discordant with the orthogonal **evolution** of diplomonads suggested on the basis of **comparative** morphology. In neighbor-joining reconstructions G. lamblia gap2 occupies a variable position, due to its great divergence. In **parsimony** and maximum likelihood analysis however, it shares a most recent common **ancestor** with the typical G. lamblia gap1 gene, suggesting that it diverged after the separation of the Giardia lineage. The position of the diplomonad clade in broader **phylogenetic** reconstructions is firmly within the typical cytosolic glycolytic representatives of GAPDH of eukaryotes.

L13 ANSWER 54 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI Reconstruction of **ancestral sequences** by the inferential method, a tool for protein engineering studies.
ACCESSION NUMBER: 1994:435342 BIOSIS
DOCUMENT NUMBER: PREV199497448342
TITLE: Reconstruction of **ancestral sequences** by the inferential method, a tool for protein engineering studies.
AUTHOR(S): Libertini, Giacinto; Di Donato, Alberto (1)
CORPORATE SOURCE: (1) Dep. Organic Biol. Chem., Univ. Naples Federico II, via Mezzocannone 16, 80134 Naples Italy
SOURCE: Journal of Molecular Evolution, (1994) Vol. 39, No. 2, pp. 219-229.
ISSN: 0022-2844.
DOCUMENT TYPE: Article
LANGUAGE: English
AB This paper describes the inferential method, an approach for reconstructing protein and nucleotide **sequences** of **ancestral** species, starting from known, homologous, contemporary **sequences**. The method requires knowledge of the topology of the **phylogenetic** tree, whose nodes are the species to whom the reconstructed **sequences** belong. The method has been tested by computer simulation of speciation and nucleotide substitutions, starting from a single **ancestral sequence**, and by subsequent reconstruction of nodal **sequences**. Results have shown that reconstructions obtained by the inferential method are affected by limited error frequencies, which (1) are proportional to the squares of nucleotide substitution rates and of internodal distances, and (2) are little influenced by non-uniformity of transformation rates of nucleotides. Furthermore, good agreement of the results has been obtained by **comparing** protein-**sequence** reconstructions carried out with the inferential method with those obtained using the maximum **parsimony** method in two different cases: e.g., a reconstruction of simulated **sequences** and a reconstruction of mammalian ribonuclease **sequences**.

L13 ANSWER 56 OF 62 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
TI **Phylogenetic** Relationships in the honeybee (Genus Apis) as determined by the **sequence** of the cytochrome oxidase II region of mitochondrial DNA.
ACCESSION NUMBER: 1994:437366 BIOSIS
DOCUMENT NUMBER: PREV199497450366
TITLE: **Phylogenetic** Relationships in the honeybee (Genus Apis) as determined by the **sequence** of the cytochrome oxidase II region of mitochondrial DNA.
AUTHOR(S): Willis, Leslie G. (1); Winston, Mark L.; Honda, Barry M.
CORPORATE SOURCE: (1) Dep. Biol. Sci., Simon Fraser Univ., Burnaby, BC V5A 1S6 Canada
SOURCE: Molecular Phylogenetics and Evolution, (1992) Vol. 1, No. 3, pp. 169-178.
ISSN: 1055-7903.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The complete nucleotide **sequence** of the mitochondrial cytochrome oxidase II (COII) gene was determined for five species of the honeybee (Genus: Apis): A. andreniformis, A. cerana, A. dorsata, A. florea, and A. koschevnikovi; these were then **compared** to the known **sequence** of the A. millifera gene from Crozier et al. (1989, Mol. Biol. **Evol**., 6: 399-411) and the wasp Excristes roborator (Liu and Beckenbach, 1992, Mol. **Phylogenet**. **Evol**., 1:41-52). **Phylogenetic** relationships were derived using the **parsimony** methods DNAPARS and PROTPARS of Felsenstein ("PHYLIP Manual Version 3.4, "University Herbarium, Univ. of California, Berkeley). The results suggest that A. dorsata is the most **ancestral** species, followed by the branching of A. Borea/A. andreniformis and A. koschevnikovi, and then A. mellifera and A. cerana. This inference differs from the currently accepted view that considers the A. florea/A. andreniformis line to be the most **ancestral**.

L13 ANSWER 57 OF 62 MEDLINE DUPLICATE 14
TI **Evolution** of RNA polymerases and branching patterns of the three major groups of Archaebacteria.
ACCESSION NUMBER: 91186417 MEDLINE
DOCUMENT NUMBER: 91186417 PubMed ID: 1901370
TITLE: **Evolution** of RNA polymerases and branching patterns of the three major groups of Archaebacteria.
AUTHOR: Iwabe N; Kuma K; Kishino H; Hasegawa M; Miyata T
CORPORATE SOURCE: Department of Biology, Faculty of Science, Kyushu University, Fukuoka, Japan.
SOURCE: JOURNAL OF MOLECULAR EVOLUTION, (1991 Jan) 32 (1) 70-8. Journal code: 0360051. ISSN: 0022-2844.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199105
ENTRY DATE: Entered STN: 19910526
Last Updated on STN: 19980206
Entered Medline: 19910506
AB The amino acid **sequences** of the largest subunits of the RNA polymerases I, II, and III from eukaryotes were **compared** with those of archaebacterial and eubacterial homologs, and their **evolutionary** relationships were analyzed in detail by a recently developed tree-making method, the likelihood method of protein **phylogeny**, as well as by the neighbor-joining method and the **parsimony** method, together with bootstrap analyses. It was shown that the best tree topologies predicted by the first two methods are identical, whereas the last one predicts a distinct tree. The maximum likelihood tree revealed that, after the separation from archaebacteria, the three eukaryotic RNA polymerases diverged from an **ancestral** precursor in the eukaryotic lineage. This result is contrasted with the published result showing multiple origins for the three eukaryotic polymerases. It was shown that eukaryotic RNA polymerase I **evolved** much more rapidly than RNA polymerases II and III: The N-terminal half of RNA polymerase I shows an extraordinarily high **evolutionary** rate, possibly due to relaxed functional constraints. In contrast the **evolutionary** rate of archaebacterial RNA polymerase is remarkably limited. In addition, including the second largest subunit of the RNA polymerase, a detailed analysis for the branching pattern of the three major groups of archaebacteria was carried out by the maximum likelihood method. It was shown that the three major groups of archaebacteria are likely to form a single cluster; that is, archaebacteria are likely to be monophyletic as originally proposed by Woese and his colleagues.

L13 ANSWER 62 OF 62 FEDRIP COPYRIGHT 2002 NTIS
TI **EVOLUTIONARY** RELATIONSHIPS AND GENETIC CHARACTERIZATION OF PSYLLID ENDOSYMBIONTS
ACCESSION NUMBER: 2002:113119 FEDRIP

NUMBER OF REPORT: AGRIC 0180815
RESEARCH TITLE: **EVOLUTIONARY** RELATIONSHIPS AND GENETIC CHARACTERIZATION OF PSYLLID ENDOSYMBIONTS
STAFF Baumann, P.
PERFORMING ORGN: UNIV OF CALIFORNIA, MICROBIOLOGY, DAVIS, CALIFORNIA, 95616
FUNDING: HATCH |c H
FILE SEGMENT: Department of Agriculture

SUM Most psyllids appear to have two types of enodsymbionts. We are interested in establishing the **evolutionary** relationship of these endosymbionts by means of 16S rDNA analysis and determining whether the endosymbionts are the result of a single infection or multiple infections. If one of the endosymbionts is the result of a single infection we will determine if it has genes for the biosynethesis of amino acids and if any of these are amplied by being on plasmids. Standard molecular biology techniques will be used to amplify 16S rDNA, clone into plasmid vectors and determine its **sequence**. **Phylogenetic** analysis will be performed by **parsimony** methods. Endosymbionts will be purified by a combination of filtration and Percol gradients. Probes will be devised for genes encoding **enzymes** of amino acid biosynethesis. Using these probes restriction **enzyme** and Southern blot analyses will be performed. The appropriate fragments will be cloned and **sequenced** and the genes present determined by **sequence comparisons** with data bases.PR contain primary endosymbionts, designated as Candidatus Carsonella ruddii, that cospeciate with the psyllid host. This association appears to be the consequence of a single infection of a psyllid **ancestor** with a bacterium. Some psyllids may have additional secondary (S-) endosymbionts. We have cloned and **sequenced** the 16S-23S ribosomal RNA genes of seven representative psyllid S-endosymbionts. **Comparisons** of the S-endosymbiont **phylogenetic** trees with those of C. ruddii indicate a lack of congruence, a finding consistent with multiple infections of psyllids with different precursors of the S-endosymbionts and possible horizontal transmission. Additional **comparisons** indicate that the S-endosymbionts are related to members of the Enterobacteriaceae as well as to several other endosymbionts and insect-associated bacteria. Previous **phylogenetic** analyses based on endosymbiont 16S-23S ribosomal DNA and a host gene were concordant. Additional analyses using atpAGD and rpoBC gave similar trees showing the agreement expected from organisms that **evolve** through vertical transmission with no gene exchange.PB P. Baumann. 2000. Cospeciation of psyllids and their prokaryotic endosymbionts. Applied and Environmental Microbiology 66:2898-2905.PB Baumann. 2000. Secondary endosymbionts of psyllids have been acquired multiple times. Current Microbiology 41: 300-304.

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(FILE 'HOME' ENTERED AT 19:28:30 ON 06 DEC 2002)

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SEA THERMOSTA? AND EVOLUTI? AND DEHYDROGENAS?

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23	FILE BIOSIS
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6	FILE BIOTECHDS
14	FILE BIOTECHNO
1	FILE CABA

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                 1   FILE CEN
               131   FILE DGENE
                22   FILE EMBASE
                 9   FILE ESBIOBASE
                 1   FILE FEDRIP
                 3   FILE GENBANK
                 1   FILE IFIPAT
                 5   FILE JICST-EPLUS
                13   FILE LIFESCI
                16   FILE MEDLINE
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L3            324 S THERMOSTAB? AND ANCEST? AND EVOLUTI?
L4            170 S L2 AND ANCEST?
L5            154 DUP REM L4 (16 DUPLICATES REMOVED)
L6            176 S L3 AND PHYLOG?
L7            157 DUP REM L6 (19 DUPLICATES REMOVED)
L8            130 S L5 AND PHYLOG?
L9          14345 S PARSIMON? AND EVOL? AND PHYLOG?
L10          3954 S L9 AND SEQUEN? AND COMPAR?
L11           792 S L10 AND ANCEST?
L12           124 S L11 AND ENZYM?
L13            62 DUP REM L12 (62 DUPLICATES REMOVED)

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